

*John* *J/S*

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

*10/049,967C*

Source:

*101PCP*

Date Processed by STIC:

*01/21/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U S PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office; and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<http://www.uspto.gov/cbc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U S Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/049,967C

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY FTO SOFTWARE**

- 1 Wrapped Nucleic Acid Lines The number(s) at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Acid Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contains n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:
  - (1) INFORMATION FOR SEQ ID NO X (where X is shown)
  - (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
  - (ii) SEQUENCE DESCRIPTION SEQ ID NO X (where X is shown)
 This sequence is intentionally skipped.
 

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence.
- 8 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:
  - <210> sequence id number
  - <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <211> Response Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown or Artificial Sequence.
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> feature and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (See 1.823 of Sequence Rules).
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/049,967C

DATE: 06/02/2005  
TIME: 08:23:10

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\06022005\J049967C.raw

2 <110> APPLICANT: Imperial College Innovations Limited  
W--> 3 <120> TITLE OF INVENTION: Isoforms of Snare Molecules and the Uses Thereof in  
W--> 4 Modulation of Cellular Exocytosis  
W--> 5 <130> FILE REFERENCE: ICOY/P23294PC  
W--> 6 <140> CURRENT APPLICATION NUMBER: US/10/049,967C  
7 <141> CURRENT FILING DATE: 2002-02-18  
W--> 8 <160> NUMBER OF SEQ ID: 28  
9 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

26 <210> SEQ ID NO: 3 <sup>3</sup>-Found 28  
27 <211> LENGTH: 29  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Artificial Sequence  
W--> 30 <220> FEATURE:  
31 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer

W--> 32 <400> SEQUENCE: 3

E--> 33 ~~catacttgtt gcagctgcgt tggcttcat~~ 29-28

34 <210> SEQ ID NO: 4

35 <211> LENGTH: 30

36 <212> TYPE: DNA

37 <213> ORGANISM: Artificial Sequence

W--> 38 <220> FEATURE:

39 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer

W--> 40 <400> SEQUENCE: 4 <sup>30</sup>~~30~~ delete

E--> 41 ~~catacttgtt gcctttgcgt tggcttcat~~ 29

42 <210> SEQ ID NO: 5

43 <211> LENGTH: 32

44 <212> TYPE: DNA

45 <213> ORGANISM: Artificial Sequence

W--> 46 <220> FEATURE:

47 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer

W--> 48 <400> SEQUENCE: 5

E--> 49 ~~agccatcttg ttacccacca gtttgttta~~ 32-31

162 <210> SEQ ID NO: 20

163 <211> LENGTH: 10

164 <212> TYPE: PRT

165 <213> ORGANISM: Homo Sapiens

168 <400> SEQUENCE: 20

169 Gln Arg Ala Thr Lys Met Lau Gly Ser Gly

E--> 170 | | 5 10 10

Does Not Comply  
Corrected Diskette Needed  
(Pg. 1-2) ↵

pls group amino acids  
in sets of 10s

For ex: 29  
atgcctgtgc aatgtgtc 20

pls group amino  
acids in sets of  
10s. For ex: 31

aatgtgtc attcaggta

See item #3 on error summary  
sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/049,967C

DATE: 06/02/2005  
TIME: 08:23:10

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\06022005\J049967C.raw

171 <210> SEQ ID NO: 21  
 172 <211> LENGTH: 10  
 173 <212> TYPE: PRT  
 174 <213> ORGANISM: Artificial Sequence  
**W--> 175 <220> FEATURE:**  
 176 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized  
**W--> 177 <400> SEQUENCE: 21**  
 178 Gln Thr Ala Thr Lys Met Leu Gly Ser Gly  
**E--> 179 | x S 5 10 x** *K*  
 216 <210> SEQ ID NO: 26  
 217 <211> LENGTH: 5  
 218 <212> TYPE: PRT  
 219 <213> ORGANISM: Artificial Sequence  
**W--> 220 <220> FEATURE:**  
 221 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized  
 224 <400> SEQUENCE: 26  
 225 Gln Arg Ala Thr Lys  
**E--> 226 | x 5** *See item #3*  
 227 <210> SEQ ID NO: 27  
 228 <211> LENGTH: 5  
 229 <212> TYPE: PRT  
 230 <213> ORGANISM: Artificial Sequence  
**W--> 231 <220> FEATURE:**  
 232 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized  
**W--> 233 <400> SEQUENCE: 27**  
 234 Gln Thr Ala Thr Lys  
**E--> 235 | x 5** *on error summary sheet*

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/049,967C

DATE: 06/02/2005

TIME: 08:23:11

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:283 W: Missing Blank Line separator, <140> field identifier  
L:8 M:283 W: Missing Blank Line separator, <160> field identifier  
L:10 M:283 W: Missing Blank Line separator, <210> field identifier  
L:14 M:283 W: Missing Blank Line separator, <220> field identifier  
L:16 M:283 W: Missing Blank Line separator, <400> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:24 M:283 W: Missing Blank Line separator, <400> field identifier  
L:30 M:283 W: Missing Blank Line separator, <220> field identifier  
L:32 M:283 W: Missing Blank Line separator, <400> field identifier  
L:33 M:254 E: No. of Bases conflict, LENGTH:Input:29 Counted:28 SEQ:3  
L:33 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:28 SEQ:3  
L:38 M:283 W: Missing Blank Line separator, <220> field identifier  
L:40 M:283 W: Missing Blank Line separator, <400> field identifier  
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:4  
L:41 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:29 SEQ:4  
L:46 M:283 W: Missing Blank Line separator, <220> field identifier  
L:48 M:283 W: Missing Blank Line separator, <400> field identifier  
L:49 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:31 SEQ:5  
L:49 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:31 SEQ:5  
L:54 M:283 W: Missing Blank Line separator, <220> field identifier  
L:56 M:283 W: Missing Blank Line separator, <400> field identifier  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:64 M:283 W: Missing Blank Line separator, <400> field identifier  
L:70 M:283 W: Missing Blank Line separator, <220> field identifier  
L:72 M:283 W: Missing Blank Line separator, <400> field identifier  
L:78 M:283 W: Missing Blank Line separator, <220> field identifier  
L:80 M:283 W: Missing Blank Line separator, <400> field identifier  
L:86 M:283 W: Missing Blank Line separator, <220> field identifier  
L:88 M:283 W: Missing Blank Line separator, <400> field identifier  
L:94 M:283 W: Missing Blank Line separator, <220> field identifier  
L:96 M:283 W: Missing Blank Line separator, <400> field identifier  
L:102 M:283 W: Missing Blank Line separator, <220> field identifier  
L:104 M:283 W: Missing Blank Line separator, <400> field identifier  
L:110 M:283 W: Missing Blank Line separator, <220> field identifier  
L:112 M:283 W: Missing Blank Line separator, <400> field identifier  
L:118 M:283 W: Missing Blank Line separator, <220> field identifier  
L:120 M:283 W: Missing Blank Line separator, <400> field identifier  
L:126 M:283 W: Missing Blank Line separator, <220> field identifier  
L:128 M:283 W: Missing Blank Line separator, <400> field identifier  
L:134 M:283 W: Missing Blank Line separator, <220> field identifier  
L:136 M:283 W: Missing Blank Line separator, <400> field identifier  
L:142 M:283 W: Missing Blank Line separator, <220> field identifier  
L:144 M:283 W: Missing Blank Line separator, <400> field identifier  
L:150 M:283 W: Missing Blank Line separator, <220> field identifier  
L:152 M:283 W: Missing Blank Line separator, <400> field identifier  
L:158 M:283 W: Missing Blank Line separator, <220> field identifier

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/049,967C

DATE: 06/02/2005

TIME: 08:23:11

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

L:160 M:283 W: Missing Blank Line separator, <400> field identifier  
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20 ✓  
L:175 M:283 W: Missing Blank Line separator, <220> field identifier  
L:177 M:283 W: Missing Blank Line separator, <400> field identifier  
L:179 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21 ✓  
L:184 M:283 W: Missing Blank Line separator, <220> field identifier  
L:186 M:283 W: Missing Blank Line separator, <400> field identifier  
L:193 M:283 W: Missing Blank Line separator, <220> field identifier  
L:195 M:283 W: Missing Blank Line separator, <400> field identifier  
L:202 M:283 W: Missing Blank Line separator, <220> field identifier  
L:226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26 ✓  
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27 ✓

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